



012627-009.ST25

SEQUENCE LISTING

<110> ROEWKAMP, Walter  
ROSE-JOHN, Stefan

<120> CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN PROTEINS

<130> 012627-009

<140> 09/142,471

<141> 1998-11-04

<150> PCT/DE97/00458

<151> 1997-03-07

<150> DE 196 08 813.5

<151> 1996-03-07

<160> 16

<170> PatentIn Ver. 2.0

<210> 1

<211> 1627

<212> DNA

<213> Unknown

<220>

<221> sig\_peptide

<222> (34)..(90)

<220>

<221> mat\_peptide

<222> (91)..(1608)

<220>

<221> CDS

<222> (34)..(1608)

<220>

<223> Description of Unknown Organism: A conjugate  
comprising two polypeptides with a mutual  
affinity.

<400> 1

gtcgacgcat ggagtggtag ccgaggagga agc atg ctg gcc gtc ggc tgc gcg 54  
Met Leu Ala Val Gly Cys Ala

-15

ctg ctg gct gcc ctg ctg gcc gcg ccg gga gcg gcg ctg gcc cca agg 102

Leu Leu Ala Ala Leu Leu Ala Ala Pro Gly Ala Ala Leu Ala Pro Arg  
 -10 -5 -1 1

cgc tgc cct gcg cag gag gtg gca aga ggc gtg ctg acc agt ctg cca 150  
 Arg Cys Pro Ala Gln Glu Val Ala Arg Gly Val Leu Thr Ser Leu Pro  
 5 10 15 20

gga gac agc gtg act ctg acc tgc ccg ggg gta gag ccg gaa gac aat 198  
 Gly Asp Ser Val Thr Leu Thr Cys Pro Gly Val Glu Pro Glu Asp Asn  
 25 30 35

gcc act gtt cac tgg gtg ctc agg aag ccg gct gca ggc tcc cac ccc 246  
 Ala Thr Val His Trp Val Leu Arg Lys Pro Ala Ala Gly Ser His Pro  
 40 45 50

agc aga tgg gct ggc atg gga agg agg ctg ctg ctg agg tcg gtg cag 294  
 Ser Arg Trp Ala Gly Met Gly Arg Arg Leu Leu Leu Arg Ser Val Gln  
 55 60 65

ctc cac gac tct gga aac tat tca tgc tac cgg gcc ggc cgc cca gct 342  
 Leu His Asp Ser Gly Asn Tyr Ser Cys Tyr Arg Ala Gly Arg Pro Ala  
 70 75 80

ggg act gtg cac ttg ctg gtg gat gtt ccc ccc gag gag ccc cag ctc 390  
 Gly Thr Val His Leu Leu Val Asp Val Pro Pro Glu Glu Pro Gln Leu  
 85 90 95 100

tcc tgc ttc cgg aag agc ccc ctc agc aat gtt gtt tgt gag tgg ggt 438  
 Ser Cys Phe Arg Lys Ser Pro Leu Ser Asn Val Val Cys Glu Trp Gly  
 105 110 115

cct cgg agc acc cca tcc ctg acg aca aag gct gtg ctc ttg gtg agg 486  
 Pro Arg Ser Thr Pro Ser Leu Thr Thr Lys Ala Val Leu Leu Val Arg  
 120 125 130

aag ttt cag aac agt ccg gcc gaa gac ttc cag gag ccg tgc cag tat 534  
 Lys Phe Gln Asn Ser Pro Ala Glu Asp Phe Gln Glu Pro Cys Gln Tyr  
 135 140 145

tcc cag gag tcc cag aag ttc tcc tgc cag tta gca gtc ccg gag gga 582  
 Ser Gln Glu Ser Gln Lys Phe Ser Cys Gln Leu Ala Val Pro Glu Gly  
 150 155 160

gac agc tct ttc tac ata gtg tcc atg tgc gtc gcc agt agt gtc ggg 630  
 Asp Ser Ser Phe Tyr Ile Val Ser Met Cys Val Ala Ser Ser Val Gly  
 165 170 175 180

agc aag ttc agc aaa act caa acc ttt cag ggt tgt gga atc ttg cag 678  
 Ser Lys Phe Ser Lys Thr Gln Thr Phe Gln Gly Cys Gly Ile Leu Gln  
 185 190 195

cct gat ccg cct gcc aac atc aca gtc act gcc gtg gcc aga aac ccc	726
Pro Asp Pro Pro Ala Asn Ile Thr Val Thr Ala Val Ala Arg Asn Pro	
200 205 210	
cgc tgg ctc agt gtc acc tgg caa gac ccc cac tcc tgg aac tca tct	774
Arg Trp Leu Ser Val Thr Trp Gln Asp Pro His Ser Trp Asn Ser Ser	
215 220 225	
ttc tac aga cta cgg ttt gag ctc aga tat cgg gct gaa cgg tca aag	822
Phe Tyr Arg Leu Arg Phe Glu Leu Arg Tyr Arg Ala Glu Arg Ser Lys	
230 235 240	
aca ttc aca aca tgg atg gtc aag gac ctc cag cat cac tgt gtc atc	870
Thr Phe Thr Thr Trp Met Val Lys Asp Leu Gln His His Cys Val Ile	
245 250 255 260	
cac gac gcc tgg agc ggc ctg agg cac gtg gtg cag ctt cgt gcc cag	918
His Asp Ala Trp Ser Gly Leu Arg His Val Val Gln Leu Arg Ala Gln	
265 270 275	
gag gag ttc ggg caa ggc gag tgg agc gag tgg agc ccg gag gcc atg	966
Glu Glu Phe Gly Gln Gly Glu Trp Ser Glu Trp Ser Pro Glu Ala Met	
280 285 290	
ggc acg cct tgg aca gaa tcc agg agt cct cca gct cga gga ggt gga	1014
Gly Thr Pro Trp Thr Glu Ser Arg Ser Pro Pro Ala Arg Gly Gly Gly	
295 300 305	
ggt tct gga ggt gga ggt tct gga ggt gga ggt tct gtc gag cca gta	1062
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Val Glu Pro Val	
310 315 320	
ccc cca gga gaa gat tcc aaa gat gta gcc gcc cca cac aga cag cca	1110
Pro Pro Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro	
325 330 335 340	
ctc acc tct tca gaa cga att gac aaa caa att cgg tac atc ctc gac	1158
Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp	
345 350 355	
ggc atc tca gcc ctg aga aag gag aca tgt aac aag agt aac atg tgt	1206
Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys	
360 365 370	
gaa agc agc aaa gag gca ctg gca gaa aac aac ctg aac ctt cca aag	1254
Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys	
375 380 385	
atg gct gaa aaa gat gga tgc ttc caa tct gga ttc aat gag gag act	1302
Met Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr	
390 395 400	

E2  
Cont

tgc ctg gtg aaa atc atc act ggt ctt ttg gag ttt gag gta tac cta 1350  
 Cys Leu Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu  
 405 410 415 420

gag tac ctc cag aac aga ttt gag agt agt gag gaa caa gcc aga gct 1398  
 Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala  
 425 430 435

gtg cag atg agt aca aaa gtc ctg atc cag ttc ctg cag aaa aag gca 1446  
 Val Gln Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala  
 440 445 450

aag aat cta gat gca ata acc acc cct gac cca acc aca aat gcc agc 1494  
 Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser  
 455 460 465

ctg ctg acg aag ctg cag gca cag aac cag tgg ctg cag gac atg aca 1542  
 Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr  
 470 475 480

act cat ctc att ctg cgc agc ttt aag gag ttc ctg cag tcc agc ctg 1590  
 Thr His Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu  
 485 490 495 500

agg gct ctt cgg caa atg tagcatgggc accgtcgac 1627  
 Arg Ala Leu Arg Gln Met  
 505

<210> 2  
 <211> 525  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism: A conjugate  
 comprising two polypeptides with a mutual  
 affinity.

<400> 2  
 Met Leu Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro  
 -15 -10 -5

Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg  
 -1 1 5 10

Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro  
 15 20 25

Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys

E<sup>2</sup>  
Cont

<210>	3
<211>	1612
<212>	DNA
<213>	Unknown

- 6 -

&lt;220&gt;

&lt;221&gt; mat\_peptide

&lt;222&gt; (91)..(1593)

&lt;220&gt;

<223> Description of Unknown Organism:A conjugate  
comprising two polypeptides with a mutual  
affinity.

&lt;400&gt; 3

```

gtcgcacgcat ggagtggtag ccgaggagga agc atg ctg gcc gtc ggc tgc gcg 54
                               Met Leu Ala Val Gly Cys Ala
                                   -15

ctg ctg gct gcc ctg ctg gcc gcg ccg gga gcg gcg ctg gcc cca agg 102
Leu Leu Ala Ala Leu Leu Ala Ala Pro Gly Ala Ala Leu Ala Pro Arg
      -10                -5                -1  1

cgc tgc cct gcg cag gag gtg gca aga ggc gtg ctg acc agt ctg cca 150
Arg Cys Pro Ala Gln Glu Val Ala Arg Gly Val Leu Thr Ser Leu Pro
      5                10                15                20

gga gac agc gtg act ctg acc tgc ccg ggg gta gag ccg gaa gac aat 198
Gly Asp Ser Val Thr Leu Thr Cys Pro Gly Val Glu Pro Glu Asp Asn
                25                30                35

gcc act gtt cac tgg gtg ctc agg aag ccg gct gca ggc tcc cac ccc 246
Ala Thr Val His Trp Val Leu Arg Lys Pro Ala Ala Gly Ser His Pro
                40                45                50

agc aga tgg gct ggc atg gga agg agg ctg ctg ctg agg tgc gtg cag 294
Ser Arg Trp Ala Gly Met Gly Arg Arg Leu Leu Leu Arg Ser Val Gln
      55                60                65

ctc cac gac tct gga aac tat tca tgc tac ccg gcc ggc cgc cca gct 342
Leu His Asp Ser Gly Asn Tyr Ser Cys Tyr Arg Ala Gly Arg Pro Ala
      70                75                80

ggg act gtg cac ttg ctg gtg gat gtt ccc ccc gag gag ccc cag ctc 390
Gly Thr Val His Leu Leu Val Asp Val Pro Pro Glu Glu Pro Gln Leu
      85                90                95                100

tcc tgc ttc cgg aag agc ccc ctc agc aat gtt gtt tgt gag tgg ggt 438
Ser Cys Phe Arg Lys Ser Pro Leu Ser Asn Val Val Cys Glu Trp Gly
                105                110                115

cct cgg agc acc cca tcc ctg acg aca aag gct gtg ctc ttg gtg agg 486
Pro Arg Ser Thr Pro Ser Leu Thr Thr Lys Ala Val Leu Leu Val Arg
                120                125                130

aag ttt cag aac agt ccg gcc gaa gac ttc cag gag ccg tgc cag tat 534

```

E2  
Cont

Lys	Phe	Gln	Asn	Ser	Pro	Ala	Glu	Asp	Phe	Gln	Glu	Pro	Cys	Gln	Tyr		
	135						140					145					
tcc	cag	gag	tcc	cag	aag	ttc	tcc	tgc	cag	tta	gca	gtc	ccg	gag	gga	582	
Ser	Gln	Glu	Ser	Gln	Lys	Phe	Ser	Cys	Gln	Leu	Ala	Val	Pro	Glu	Gly		
	150					155					160						
gac	agc	tct	ttc	tac	ata	gtg	tcc	atg	tgc	gtc	gcc	agt	agt	gtc	ggg	630	
Asp	Ser	Ser	Phe	Tyr	Ile	Val	Ser	Met	Cys	Val	Ala	Ser	Ser	Val	Gly		
	165				170					175					180		
agc	aag	ttc	agc	aaa	act	caa	acc	ttt	cag	ggg	tgt	gga	atc	ttg	cag	678	
Ser	Lys	Phe	Ser	Lys	Thr	Gln	Thr	Phe	Gln	Gly	Cys	Gly	Ile	Leu	Gln		
				185					190					195			
cct	gat	ccg	cct	gcc	aac	atc	aca	gtc	act	gcc	gtg	gcc	aga	aac	ccc	726	
Pro	Asp	Pro	Pro	Ala	Asn	Ile	Thr	Val	Thr	Ala	Val	Ala	Arg	Asn	Pro		
			200					205					210				
cgc	tgg	ctc	agt	gtc	acc	tgg	caa	gac	ccc	cac	tcc	tgg	aac	tca	tct	774	
Arg	Trp	Leu	Ser	Val	Thr	Trp	Gln	Asp	Pro	His	Ser	Trp	Asn	Ser	Ser		
	215					220						225					
ttc	tac	aga	cta	cgg	ttt	gag	ctc	aga	tat	cgg	gct	gaa	cgg	tca	aag	822	
Phe	Tyr	Arg	Leu	Arg	Phe	Glu	Leu	Arg	Tyr	Arg	Ala	Glu	Arg	Ser	Lys		
	230				235					240							
aca	ttc	aca	aca	tgg	atg	gtc	aag	gac	ctc	cag	cat	cac	tgt	gtc	atc	870	
Thr	Phe	Thr	Thr	Trp	Met	Val	Lys	Asp	Leu	Gln	His	His	Cys	Val	Ile		
	245				250				255					260			
cac	gac	gcc	tgg	agc	ggc	ctg	agg	cac	gtg	gtg	cag	ctt	cgt	gcc	cag	918	
His	Asp	Ala	Trp	Ser	Gly	Leu	Arg	His	Val	Val	Gln	Leu	Arg	Ala	Gln		
				265				270					275				
gag	gag	ttc	ggg	caa	ggc	gag	tgg	agc	gag	tgg	agc	ccg	gag	gcc	atg	966	
Glu	Glu	Phe	Gly	Gln	Gly	Glu	Trp	Ser	Glu	Trp	Ser	Pro	Glu	Ala	Met		
		280					285					290					
ggc	acg	cct	tgg	aca	gaa	tcc	agg	agt	cct	cca	gct	cga	gga	ggg	gga	1014	
Gly	Thr	Pro	Trp	Thr	Glu	Ser	Arg	Ser	Pro	Pro	Ala	Arg	Gly	Gly	Gly		
		295				300						305					
ggg	tct	gga	ggg	gga	ggg	tct	gtc	gag	cca	gta	ccc	cca	gga	gaa	gat	1062	
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Val	Glu	Pro	Val	Pro	Pro	Gly	Glu	Asp		
	310					315					320						
tcc	aaa	gat	gta	gcc	gcc	cca	cac	aga	cag	cca	ctc	acc	tct	tca	gaa	1110	
Ser	Lys	Asp	Val	Ala	Ala	Pro	His	Arg	Gln	Pro	Leu	Thr	Ser	Ser	Glu		
	325				330					335					340		



cga att gac aaa caa att cgg tac atc ctc gac ggc atc tca gcc ctg	1158
Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu	
345 350 355	
aga aag gag aca tgt aac aag agt aac atg tgt gaa agc agc aaa gag	1206
Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu	
360 365 370	
gca ctg gca gaa aac aac ctg aac ctt cca aag atg gct gaa aaa gat	1254
Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp	
375 380 385	
gga tgc ttc caa tct gga ttc aat gag gag act tgc ctg gtg aaa atc	1302
Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile	
390 395 400	
atc act ggt ctt ttg gag ttt gag gta tac cta gag tac ctc cag aac	1350
Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn	
405 410 415 420	
aga ttt gag agt agt gag gaa caa gcc aga gct gtg cag atg agt aca	1398
Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr	
425 430 435	
aaa gtc ctg atc cag ttc ctg cag aaa aag gca aag aat cta gat gca	1446
Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala	
440 445 450	
ata acc acc cct gac cca acc aca aat gcc agc ctg ctg acg aag ctg	1494
Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu	
455 460 465	
cag gca cag aac cag tgg ctg cag gac atg aca act cat ctc att ctg	1542
Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu	
470 475 480	
cgc agc ttt aag gag ttc ctg cag tcc agc ctg agg gct ctt cgg caa	1590
Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Arg Ala Leu Arg Gln	
485 490 495 500	
atg tagcatgggc accgtcgac	1612
Met	

&lt;210&gt; 4

&lt;211&gt; 520

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Description of Unknown Organism:A conjugate

comprising two polypeptides with a mutual affinity.

<400> 4

Met	Leu	Ala	Val	Gly	Cys	Ala	Leu	Leu	Ala	Ala	Leu	Leu	Ala	Ala	Pro	-15	-10	-5	
Gly	Ala	Ala	Leu	Ala	Pro	Arg	Arg	Cys	Pro	Ala	Gln	Glu	Val	Ala	Arg	-1	1	5	10
Gly	Val	Leu	Thr	Ser	Leu	Pro	Gly	Asp	Ser	Val	Thr	Leu	Thr	Cys	Pro	15	20	25	
Gly	Val	Glu	Pro	Glu	Asp	Asn	Ala	Thr	Val	His	Trp	Val	Leu	Arg	Lys	30	35	40	45
Pro	Ala	Ala	Gly	Ser	His	Pro	Ser	Arg	Trp	Ala	Gly	Met	Gly	Arg	Arg	50	55	60	
Leu	Leu	Leu	Arg	Ser	Val	Gln	Leu	His	Asp	Ser	Gly	Asn	Tyr	Ser	Cys	65	70	75	
Tyr	Arg	Ala	Gly	Arg	Pro	Ala	Gly	Thr	Val	His	Leu	Leu	Val	Asp	Val	80	85	90	
Pro	Pro	Glu	Glu	Pro	Gln	Leu	Ser	Cys	Phe	Arg	Lys	Ser	Pro	Leu	Ser	95	100	105	
Asn	Val	Val	Cys	Glu	Trp	Gly	Pro	Arg	Ser	Thr	Pro	Ser	Leu	Thr	Thr	110	115	120	125
Lys	Ala	Val	Leu	Leu	Val	Arg	Lys	Phe	Gln	Asn	Ser	Pro	Ala	Glu	Asp	130	135	140	
Phe	Gln	Glu	Pro	Cys	Gln	Tyr	Ser	Gln	Glu	Ser	Gln	Lys	Phe	Ser	Cys	145	150	155	
Gln	Leu	Ala	Val	Pro	Glu	Gly	Asp	Ser	Ser	Phe	Tyr	Ile	Val	Ser	Met	160	165	170	
Cys	Val	Ala	Ser	Ser	Val	Gly	Ser	Lys	Phe	Ser	Lys	Thr	Gln	Thr	Phe	175	180	185	
Gln	Gly	Cys	Gly	Ile	Leu	Gln	Pro	Asp	Pro	Pro	Ala	Asn	Ile	Thr	Val	190	195	200	205
Thr	Ala	Val	Ala	Arg	Asn	Pro	Arg	Trp	Leu	Ser	Val	Thr	Trp	Gln	Asp	210	215	220	
Pro	His	Ser	Trp	Asn	Ser	Ser	Phe	Tyr	Arg	Leu	Arg	Phe	Glu	Leu	Arg				

E2  
Cont

225 230 235  
 Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp  
 240 245 250  
 Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His  
 255 260 265  
 Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser  
 270 275 280 285  
 Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser  
 290 295 300  
 Pro Pro Ala Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Val Glu  
 305 310 315  
 Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg  
 320 325 330  
 Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile  
 335 340 345  
 Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn  
 350 355 360 365  
 Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu  
 370 375 380  
 Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu  
 385 390 395  
 Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val  
 400 405 410  
 Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala  
 415 420 425  
 Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys  
 430 435 440 445  
 Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn  
 450 455 460  
 Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp  
 465 470 475  
 Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser  
 480 485 490  
 Ser Leu Arg Ala Leu Arg Gln Met

495

500

&lt;210&gt; 5

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

<223> Description of Unknown Organism: A conjugate  
comprising two polypeptides with a mutual  
affinity.

&lt;400&gt; 5

Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu  
1 5 10 15

Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro Val Pro Pro  
20 25 30

Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr  
35 40 45

Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile  
50 55 60

Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser  
65 70 75 80

Ser Pro Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala  
85 90 95

Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu  
100 105 110

Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr  
115 120 125

Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln  
130 135 140

Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn  
145 150 155 160

Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu  
165 170 175

Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Glu Asp Met Pro Thr His  
180 185 190

Leu Ile Leu Arg Ser Leu Lys Glu Phe Leu Gln Arg Ser Leu Arg Ala

	195	200	205
Leu Arg Gln Met			
210			
<210> 6			
<211> 20			
<212> DNA			
<213> Sonstige Nucleinsaure			
<400> 6			
taatacgact cactataggg			20
<210> 7			
<211> 25			
<212> DNA			
<213> Sonstige Nucleinsaure			
<400> 7			
ccgctcgagc tggaggactc ctgga			25
<210> 8			
<211> 27			
<212> DNA			
<213> Sonstige Nucleinsaure			
<400> 8			
cggctcgagc cagtaccccc aggagaa			27
<210> 9			
<211> 20			
<212> DNA			
<213> Sonstige Nucleinsaure			
<400> 9			
ccacagaagt aaggttcctt			20
<210> 10			
<211> 50			
<212> DNA			
<213> Sonstige Nucleinsaure			
<400> 10			
tcgaggaggt ggaggttctg gaggtggagg ttctggaggt ggaggttctg			50

E2  
cont

<210> 11  
 <211> 50  
 <212> DNA  
 <213> Sonstige Nucleinsaure

<400> 11  
 tcgacagaac ctccacctcc agaacctcca cctccagaac ctccacctcc 50

<210> 12  
 <211> 35  
 <212> DNA  
 <213> Sonstige Nucleinsaure

<400> 12  
 tcgaggaggt ggaggttctg gaggtggagg ttctg 35

<210> 13  
 <211> 35  
 <212> DNA  
 <213> Sonstige Nucleinsaure

<400> 13  
 tcgacagaac ctccacctcc agaacctcca cctcc 35

<210> 14  
 <211> 19  
 <212> PRT  
 <213> Unknown

<220>  
 <223> a signal peptide which is a conjugate comprising  
 one of two polypeptides with a mutual affinity

<400> 14  
 Met Leu Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro  
 1 5 10 15  
 Gly Ala Ala

<210> 15  
 <211> 18  
 <212> PRT  
 <213> Unknown

<220>  
 <223> a linker peptide which is a conjugate comprising  
 one of two polypeptides with a mutual affinity

&lt;400&gt; 15

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15  
Val Glu

&lt;210&gt; 16

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

<223> a linker peptide which is a conjugate comprising  
one of two polypeptides with a mutual affinity

&lt;400&gt; 16

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Val Glu  
1 5 10

---